RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/ 757, 100_

Source: _O1PE_

Date Processed by STIC: _2 - 5 - 01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/757,100

ATTN; NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ___ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ___ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ___ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ___ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ___ Variable Length Sequence(s) ___ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 ___ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 ___ Skipped Sequences (OLD RULES) Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ___ Skipped Sequences (NEW RULES) Sequence(s) ___ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ___ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ___ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.

12 ___ Use of <220>Feature (NEW RULES) Sequence(s) ___ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 ___ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

```
RAW SEQUENCE LISTING              DATE: 02/05/2001
PATENT APPLICATION:  US/09/757,100    TIME: 14:24:27

Input Set : A:\isph-533.seq.asc
Output Set: N:\CRF3\02052001\I757100.raw
```

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       6 <110> APPLICANT: Monia, Brett P.
       7        Gaarde, William A.
       8        Nero, Pamela S.
      11 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
      12        Expression
      14 <130> FILE REFERENCE: ISPH-0533
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/757,100
C--> 17 <141> CURRENT FILING DATE: 2001-01-09
      19 <150> PRIOR APPLICATION NUMBER: 09/377,310
      20 <151> PRIOR FILING DATE: 1999-08-19
      22 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999
      23 <151> PRIOR FILING DATE: 2000-07-13
      25 <160> NUMBER OF SEQ ID NOS: 44
      27 <170> SOFTWARE: PatentIn Ver. 2.0
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ERRORED SEQUENCES

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      29 <210> SEQ ID NO: 1
      30 <211> LENGTH: 3791
      31 <212> TYPE: DNA
      32 <213> ORGANISM: Homo sapiens
      34 <220> FEATURE:
      35 <221> NAME/KEY: CDS
      36 <222> LOCATION: (233)..(3391)
      38 <300> PUBLICATION INFORMATION:
      39 <303> JOURNAL: DNA
      40 <304> VOLUME: 12
      41 <305> ISSUE: 9
      42 <306> PAGES: 823-830
W--> 43 <307> DATE: 1993-11
      44 <308> DATABASE ACCESSION NO: L13616/Genbank
      45 <309> DATABASE ENTRY DATE: 1995-01-02
      47 <400> SEQUENCE: 1
E--> 48 cgaccactgt  gagcccgcgg  cgtgaggcgt  cgggaggaag  cgcggctgct
      49 gtcgcccagc 60
E--> 51 gccgccccgt  cgtcgtctgc  cttcgcttca  cggcgccgag  ccgcggtccg
      52 agcagaactg 120
E--> 54 gggctccctt  gcatcttcca  gttacaaatt  cagtgccttc  tgcagtttcc
      55 ccagagctcc 180
E--> 57 tcaagaataa  cggaagggag  aatatgacag  atacctagca  tctagcaaaa  ta
      58 atg gca 238
      60 Met Ala
      62 1
E--> 64 gct gct tac ctt gac ccc aac ttg aat cac aca cca aat tcg agt
      65 act   286
      66 Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser Ser
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The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check subsequent sequences for similar errors.

```
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                Input Set : A:\isph-533.seq.asc
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W--> 67 Thr
W--> 68         5                10                 15
E--> 70 aag act cac ctg ggt act ggt atg gaa cgt tct cct ggt gca atg
     71 gag    334
     72 Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala Met
W--> 73 Glu
W--> 74        20                25                 30
E--> 76 cga gta tta aag gtc ttt cat tat ttt gaa agc aat agt gag cca
     77 acc    382
     78 Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu Pro
W--> 79 Thr
W--> 80        35                40                 45
E--> 81 50
E--> 83 acc tgg gcc agt att atc agg cat gga gat gct act gat gtc agg
     84 ggc    430
     85 Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val Arg
W--> 86 Gly
W--> 87             55                60                 65
E--> 89 atc att cag aag ata gtg gac agt cac aaa gta aag cat gtg gcc
     90 tgc    478
     91 Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val Ala
W--> 92 Cys
W--> 93             70                75                 80
E--> 95 tat gga ttc cgc ctc agt cac ctg cgg tca gag gag gtt cac tgg
     96 ctt    526
     97 Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His Trp
W--> 98 Leu
W--> 99         85                90                 95
E--> 101 cac gtg gat atg ggc gtc tcc agt gtg agg gag aag tat gag ctt
     102 gct    574
     103 His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu Leu
W--> 104 Ala
W--> 105     100               105                110
E--> 107 cac cca cca gag gag tgg aaa tat gaa ttg aga att cgt tat ttg
     108 cca    622
     109 His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr Leu
W--> 110 Pro
W--> 111 115               120                125
E--> 112 130
E--> 114 aaa gga ttt cta aac cag ttt act gaa gat aag cca act ttg aat
     115 ttc    670
     116 Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu Asn
W--> 117 Phe
W--> 118             135               140                145
E--> 120 ttc tat caa cag gtg aag agc gat tat atg tta gag ata gct gat
     121 caa    718
     122 Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala Asp
W--> 123 Gln
W--> 124             150               155                160
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wrapped text

```
RAW SEQUENCE LISTING              DATE: 02/05/2001
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         Input Set : A:\isph-533.seq.asc
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E--> 126 gtg gac cag gaa att gct ttg aag ttg ggt tgt cta gaa ata cgg
     127 cga    766
     128 Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile Arg
W--> 129 Arg
W--> 130         165             170             175
E--> 132 tca tac tgg gag atg cgg ggc aat gca cta gaa aag aag tct aac
     133 tat    814
     134 Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser Asn
W--> 135 Tyr
W--> 136     180             185             190
E--> 138 gaa gta tta gaa aaa gat gtt ggt tta aag cga ttt ttt cct aag
     139 agt    862
     140 Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys
W--> 141 Ser
W--> 142 195                 200             205
E--> 143 210
E--> 145 tta ctg gat tct gtc aag gcc aaa aca cta aga aaa ctg atc caa
     146 caa    910
     147 Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln
W--> 148 Gln
W--> 149             215             220             225
E--> 151 aca ttt aga caa ttt gcc aac ctt aat aga gaa gaa agt att ctg
     152 aaa    958
     153 Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu
W--> 154 Lys
W--> 155         230             235             240
E--> 157 ttc ttt gag atc ctg tct cca gtc tac aga ttt gat aag gaa tgc
     158 ttc    1006
     159 Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys
W--> 160 Phe
W--> 161         245             250             255
E--> 163 aag tgt gct ctt ggt tca agc tgg att att tca gtg gaa ctg gca
     164 atc    1054
     165 Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala
W--> 166 Ile
W--> 167     260             265             270
E--> 169 ggc cca gaa gaa gga atc agt tac cta acg gac aag ggc tgc aat
     170 ccc    1102
     171 Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn
W--> 172 Pro
W--> 173 275                 280             285
E--> 174 290
E--> 176 aca cat ctt gct gac ttc act caa gtg caa acc att cag tat tca
     177 aac    1150
     178 Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser
W--> 179 Asn
W--> 180             295             300             305
E--> 182 agt gaa gac aag gac aga aaa gga atg cta caa cta aaa ata gca
     183 ggt    1198
```

wrapped text

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        RAW SEQUENCE LISTING              DATE: 02/05/2001
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        Input Set : A:\isph-533.seq.asc
        Output Set: N:\CRF3\02052001\I757100.raw


        184 Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala
W--> 185 Gly
W--> 186          310                315                320
E--> 188 gca ccc gag cct ctg aca gtg acg gca cca tcc cta acc att gcg
     189 gag     1246
        190 Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala
W--> 191 Glu
W--> 192          325                330                335
E--> 194 aat atg gct gac cta ata gat ggg tac tgc cgg ctg gtg aat gga
     195 acc     1294
        196 Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly
W--> 197 Thr
W--> 198          340                345                350
E--> 200 tcg cag tca ttt atc atc aga cct cag aaa gaa ggt gaa cgg gct
     201 ttg     1342
        202 Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala
W--> 203 Leu
W--> 204 355                360                         365
E--> 205 370
E--> 207 cca tca ata cca aag ttg gcc aac agc gaa aag caa ggc atg cgg
     208 aca     1390
        209 Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg
W--> 210 Thr
W--> 211          375                380                385
E--> 213 cac gcc gtc tct gtg tca gaa aca gat gat tat gct gag att ata
     214 gat     1438
        215 His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile
W--> 216 Asp
W--> 217          390                395                400
E--> 219 gaa gaa gat act tac acc atg ccc tca acc agg gat tat gag att
     220 caa     1486
        221 Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile
W--> 222 Gln
W--> 223          405                410                415
E--> 225 aga gaa aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt
     226 gga     1534
        227 Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe
W--> 228 Gly
W--> 229 420                425                430
E--> 231 gat gta cat caa ggc att tat atg agt cca gag aat cca gct ttg
     232 gcg     1582
        233 Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu
W--> 234 Ala
W--> 235 435                440                         445
E--> 236 450
E--> 238 gtt gca att aaa aca tgt aaa aac tgt act tcg gac agc gtg aga
     239 gag     1630
        240 Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg
W--> 241 Glu
```

wrapped text

```
W--> 242              455              460              465
E--> 244 aaa ttt ctt caa gaa gcc tta aca atg cgt cag ttt gac cat cct
     245 cat    1678
     246 Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His Pro
W--> 247 His
W--> 248              470              475              480
E--> 250 att gtg aag ctg att gga gtc atc aca gag aat cct gtc tgg ata
     251 atc    1726
     252 Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile
W--> 253 Ile
W--> 254              485              490              495
E--> 256 atg gag ctg tgc aca ctt gga gag ctg agg tca ttt ttg caa gta
     257 agg    1774
     258 Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val
W--> 259 Arg
W--> 260     500              505              510
E--> 262 aaa tac agt ttg gat cta gca tct ttg atc ctg tat gcc tat cag
     263 ctt    1822
     264 Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln
W--> 265 Leu
W--> 266 515              520              525
E--> 267 530
E--> 269 agt aca gct ctt gca tat cta gag agc aaa aga ttt gta cac agg
     270 gac    1870
     271 Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg
W--> 272 Asp
W--> 273              535              540              545
E--> 275 att gct gct cgg aat gtt ctg gtg tcc tca aat gat tgt gta aaa
     276 tta    1918
     277 Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys
W--> 278 Leu
W--> 279              550              555              560
E--> 281 gga gac ttt gga tta tcc cga tat atg gaa gat agt act tac tac
     282 aaa    1966
     283 Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr
W--> 284 Lys
W--> 285     565              570              575
E--> 286 gct tcc aaa gga aaa ttg cct att aaa tgg atg gct cca gag tca
     287 atc    2014
     288 Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser
W--> 289 Ile
W--> 290     580              585              590
E--> 292 aat ttt cga cgt ttt acc tca gct agt gac gta tgg atg ttt ggt
     293 gtg    2062
     294 Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly
W--> 295 Val
W--> 296 595              600              605
E--> 297 610
E--> 299 tgt atg tgg gag ata ctg atg cat ggt gtg aag cct ttt caa gga
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Wrapped text

```
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          Input Set : A:\isph-533.seq.asc
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      300 gtg   2110
      301 Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly
W--> 302 Val
W--> 303           615           620           625
E--> 305 aag aac aat gat gta atc ggt cga att gaa aat ggg gaa aga tta
      306 cca   2158
      307 Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu
W--> 308 Pro
W--> 309           630           635           640
E--> 311 atg cct cca aat tgt cct cct acc ctc tac agc ctt atg acg aaa
      312 tgc   2206
      313 Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys
W--> 314 Cys
W--> 315           645           650           655
E--> 317 tgg gcc tat gac ccc agc agg cgg ccc agg ttt act gaa ctt aaa
      318 gct   2254
      319 Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys
W--> 320 Ala
W--> 321   660           665           670
E--> 323 cag ctc agc aca atc ctg gag gaa gag aag gct cag caa gaa gag
      324 cgc   2302
      325 Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu
W--> 326 Arg
W--> 327 675           680           685
E--> 328 690
E--> 330 atg agg atg gag tcc aga aga cag gcc aca gtg tcc tgg gac tcc
      331 gga   2350
      332 Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp Ser
W--> 333 Gly
W--> 334           695           700           705
E--> 336 ggg tct gat gaa gca ccg ccc aag ccc agc aga ccg ggt tat ccc
      337 agt   2398
      338 Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr Pro
W--> 339 Ser
W--> 340           710           715           720
E--> 342 ccg agg tcc agc gaa gga ttt tat ccc agc cca cag cac atg gta
      343 caa   2446
      344 Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met Val
W--> 345 Gln
W--> 346           725           730           735
E--> 348 acc aat cat tac cag gtt tct ggc tac cct ggt tca cat gga atc
      349 aca   2494
      350 Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly Ile
W--> 351 Thr
W--> 352   740           745           750
E--> 354 gcc atg gct ggc agc atc tat cca ggt cag gca tct ctt ttg gac
      355 caa   2542
      356 Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu Asp
W--> 357 Gln
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Wrapped text

```
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            Input Set : A:\isph-533.seq.asc
            Output Set: N:\CRF3\02052001\I757100.raw

W--> 358 755                    760                    765
E--> 359 770
E--> 361 aca gat tca tgg aat cat aga cct cag gag ata gca atg tgg cag
     362 ccc    2590
     363 Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp Gln
W--> 364 Pro
W--> 365               775                    780                    785
E--> 367 aat gtg gag gac tct aca gta ttg gac ctg cga ggg att ggg caa
     368 gtg    2638
     369 Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly Gln
W--> 370 Val
W--> 371               790                    795                    800
E--> 373 ttg cca acc cat ctg atg gaa gag cgt cta atc cga cag caa cag
     374 gaa    2686
     375 Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln Gln
W--> 376 Glu
W--> 377          805                    810                    815
E--> 379 atg gaa gaa gat cag cgc tgg ctg gaa aaa gag gaa aga ttt ctg
     380 aaa    2734
     381 Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe Leu
W--> 382 Lys
W--> 383          820                    825                    830
E--> 385 cct gat gtg aga ctc tct cga ggc agt att gac agg gag gat gga
     386 agt    2782
     387 Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp Gly
W--> 388 Ser
W--> 389 835                    840                    845
E--> 390 850
E--> 392 ctt cag ggt ccg att gga aac caa cat ata tat cag cct gtg ggt
     393 aaa    2830
     394 Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val Gly
W--> 395 Lys
W--> 396               855                    860                    865
E--> 398 cca gat cct gca gct cca cca aag aaa ccg cct cgc cct gga gct
     399 ccc    2878
     400 Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly Ala
W--> 401 Pro
W--> 402               870                    875                    880
E--> 404 ggt cat ctg gga agc ctt gcc agc ctc agc agc cct gct gac agc
     405 tac    2926
     406 Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp Ser
W--> 407 Tyr
W--> 408          885                    890                    895
E--> 410 aac gag ggt gtc aag ctt cag ccc cag gaa atc agc ccc cct cct
     411 act    2974
     412 Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro Pro
W--> 413 Thr
W--> 414 900                    905                    910
E--> 416 gcc aac ctg gac cgg tcg aat gat aag gtg tac gag aat gtg acg
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wrapped text

```
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                Input Set : A:\isph-533.seq.asc
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        417 ggc    3022
        418 Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val Thr
W--> 419 Gly
W--> 420 915                          920                          925
E--> 421 930
E--> 423 ctg gtg aaa gct gtc atc gag atg tcc agt aaa atc cag cca gcc
    424 cca    3070
        425 Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro Ala
W--> 426 Pro
W--> 427              935              940                          945
E--> 429 cca gag gag tat gtc cct atg gtg aag gaa gtc ggc ttg gcc ctg
    430 agg    3118
        431 Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala Leu
W--> 432 Arg
W--> 433         950              955                          960
E--> 435 aca tta ttg gcc act gtg gat gag acc att ccc ctc cta cca gcc
    436 agc    3166
        437 Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro Ala
W--> 438 Ser
W--> 439         965              970                          975
E--> 441 acc cac cga gag att gag atg gca cag aag cta ttg aac tct gac
    442 ctg    3214
        443 Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser Asp
W--> 444 Leu
W--> 445      980                 985                      990
E--> 447 ggt gag ctc atc aac aag atg aaa ctg gcc cag cag tat gtc atg
    448 acc    3262
        449 Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val Met
W--> 450 Thr
W--> 451 995                      1000                         1005
E--> 452 1010
E--> 454 agc ctc cag caa gag tac aaa aag caa atg ctg act gct gct cac
    455 gcc    3310
        456 Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala His
W--> 457 Ala
W--> 458              1015             1020                         1025
E--> 460 ctg gct gtg gat gcc aaa aac tta ctc gat gtc att gac caa gca
    461 aga    3358
        462 Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln Ala
W--> 463 Arg
W--> 464         1030             1035                    1040
E--> 466 ctg  aaa  atg  ctt ggg cag acg aga cca cac  tga  gcctcccta
    467 ggagcacgtc 3411
        468 Leu Lys Met Leu Gly Gln Thr Arg Pro His
W--> 469         1045             1050
E--> 471 ttgctaccct   cttttgaaga  tgttctctag  ccttccacca  gcagcgagga
    472 attaaccctg 3471
E--> 474 tgtcctcagt  cgccagcact  tacagctcca  actttttga  atgaccatct
    475 ggttgaaaaa 3531
```

RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/757,100   TIME: 14:24:27

                Input Set : A:\isph-533.seq.asc
                Output Set: N:\CRF3\02052001\I757100.raw

E--> 477 tctttctcat   ataagtttaa   ccacactttg   atttgggttc   atttttttgtt
     478 ttgttttttt 3591
E--> 480 caatcatgat   attcagaaaa   atccaggatc   caaaatgtgg   cgtttttcta
     481 agaatgaaaa 3651
E--> 483 ttatatgtaa   gcttttaagc   atcatgaaga   acaatttatg   ttcacattaa
     484 gatacgttct 3711
E--> 486 aaaggggat   ggccaagggg   tgacatctta   attcctaaac   taccttagct
     487 gcatagtgga 3771
E--> 489 agaggagagc   tagaagcaaa
     490 3791
     493 <210> SEQ ID NO: 2
     494 <211> LENGTH: 1052
     495 <212> TYPE: PRT
     496 <213> ORGANISM: Homo sapiens
     498 <400> SEQUENCE: 2
     499 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn
E--> 500 Ser
E--> 501   1   5   10   15
     503 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly
E--> 504 Ala
E--> 505   20   25   30
     507 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser
E--> 508 Glu
E--> 509   35   40   45
     511 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp
E--> 512 Val
E--> 513   50   55   60
     515 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His
E--> 516 Val
E--> 517   65   70   75
E--> 518 80
     520 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val
E--> 521 His
E--> 522   85   90   95
     524 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr
E--> 525 Glu
E--> 526   .   100   105   110
     528 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg
E--> 529 Tyr
E--> 530   115   120   125
     532 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr
E--> 533 Leu
E--> 534   130   135   140
     536 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile
E--> 537 Ala
E--> 538 145   150   155
E--> 539 160
     541 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu
E--> 542 Ile

wrapped text

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                RAW SEQUENCE LISTING            DATE: 02/05/2001
                PATENT APPLICATION:  US/09/757,100    TIME: 14:24:27

                Input Set : A:\isph-533.seq.asc
                Output Set: N:\CRF3\02052001\I757100.raw

E--> 543                    165                 170                 175
     545 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys
E--> 546 Ser
E--> 547           180                 185                 190
     549 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe
E--> 550 Pro
E--> 551           195                 200                 205
     553 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu
E--> 554 Ile
E--> 555           210                 215                 220
     557 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser
E--> 558 Ile
E--> 559 225                           230                           235
E--> 560 240
     562 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys
E--> 563 Glu
E--> 564           245                 250                 255
     566 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu
E--> 567 Leu
E--> 568           260                 265                 270
     570 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly
E--> 571 Cys
E--> 572           275                 280                 285
     574 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln
E--> 575 Tyr
E--> 576           290                 295                 300
     578 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys
E--> 579 Ile
E--> 580 305                           310                           315
E--> 581 320
     583 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr
E--> 584 Ile
E--> 585           325                 330                 335
     587 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val
E--> 588 Asn
E--> 589           340                 345                 350
     591 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu
E--> 592 Arg
E--> 593           355                 360                 365
     595 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly
E--> 596 Met
E--> 597           370                 375                 380
     599 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu
E--> 600 Ile
E--> 601 385                           390                           395
E--> 602 400
     604 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr
E--> 605 Glu
E--> 606           405                 410                 415
```

Wrapped text

RAW SEQUENCE LISTING   DATE: 02/05/2001
PATENT APPLICATION: US/09/757,100   TIME: 14:24:27

Input Set : A:\isph-533.seq.asc
Output Set: N:\CRF3\02052001\I757100.raw

```
      608 Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly
E--> 609 Gln
E--> 610         420             425             430
      612 Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
E--> 613 Ala
E--> 614         435             440             445
      616 Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
E--> 617 Val
E--> 618     450             455             460
      620 Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp
E--> 621 His
E--> 622 465                 470                 475
E--> 623 480
      625 Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val
E--> 626 Trp
E--> 627         485             490             495
      629 Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu
E--> 630 Gln
E--> 631         500             505             510
      633 Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala
E--> 634 Tyr
E--> 635         515             520             525
      637 Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val
E--> 638 His
E--> 639     530             535             540
      641 Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys
E--> 642 Val
E--> 643 545                 550                 555
E--> 644 560
      646 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr
E--> 647 Tyr
E--> 648         565             570             575
      650 Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro
E--> 651 Glu
E--> 652         580             585             590
      654 Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met
E--> 655 Phe
E--> 656     595             600             605
      658 Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe
E--> 659 Gln
E--> 660     610             615             620
      662 Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu
E--> 663 Arg
E--> 664 625                 630                 635
E--> 665 640
      666 Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met
E--> 667 Thr
E--> 668         645             650             655
      670 Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu
```

Wrapped Text

```
E--> 671 Leu
E--> 672           660                   665                   670
     674 Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln
E--> 675 Glu
E--> 676           675                   680                   685
     678 Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp
E--> 679 Asp
E--> 680           690                   695                   700
     682 Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly
E--> 683 Tyr
E--> 684 705                   710                   715
E--> 685 720
     687 Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His
E--> 688 Met
E--> 689           725                   730                   735
     691 Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His
E--> 692 Gly
E--> 693           740                   745                   750
     695 Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu
E--> 696 Leu
E--> 697           755                   760                   765
     699 Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met
E--> 700 Trp
E--> 701           770                   775                   780
     703 Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile
E--> 704 Gly
E--> 705 785                   790                   795
E--> 706 800
     708 Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln
E--> 709 Gln
E--> 710           805                   810                   815
     712 Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg
E--> 713 Phe
E--> 714           820                   825                   830
     716 Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu
E--> 717 Asp
E--> 718           835                   840                   845
     720 Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro
E--> 721 Val
E--> 722           850                   855                   860
     724 Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro
E--> 725 Gly
E--> 726 865                   870                   875
E--> 727 880
     729   a Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala
E--> 730 Asp
E--> 731           885                   890                   895
     733 Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro
E--> 734 Pro
```

```
               RAW SEQUENCE LISTING            DATE: 02/05/2001
               PATENT APPLICATION: US/09/757,100    TIME: 14:24:27

               Input Set : A:\isph-533.seq.asc
               Output Set: N:\CRF3\02052001\I757100.raw

E--> 735            900              905              910
     737 Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn
E--> 738 Val
E--> 739       915            920              925
     741 Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln
E--> 742 Pro
E--> 743    930              935            940
     745 Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu
E--> 746 Ala
E--> 747 945                950                    955
E--> 748 960
     750 Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu
E--> 751 Pro
E--> 752          965            970              975
     754 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn
E--> 755 Ser
E--> 756          980            985              990
     757 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr
E--> 758 Val
E--> 759       995            1000             1005
     761 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala
E--> 762 Ala
E--> 763    1010            1015             1020
     765 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp
E--> 766 Gln
E--> 767 025              1030                    1035
E--> 768 1040
     770 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
E--> 771            1045            1050
     774 <210> SEQ ID NO: 3
     775 <211> LENGTH: 20
     776 <212> TYPE: DNA
     777 <213> ORGANISM: Artificial Sequence
     779 <220> FEATURE:
     780 <223> OTHER INFORMATION: antisense sequence
     782 <400> SEQUENCE: 3
E--> 783 ccgcgggctc                    acagtggtcg
     784 20
     787 <210> SEQ ID NO: 4
     788 <211> LENGTH: 20
     789 <212> TYPE: DNA
     790 <213> ORGANISM: Artificial Sequence
     792 <220> FEATURE:
     793 <223> OTHER INFORMATION: antisense sequence
     795 <400> SEQUENCE: 4
E--> 796 ggcgccgtga                    agcgaaggca
     797 20
     800 <210> SEQ ID NO: 5
     801 <211> LENGTH: 20
```
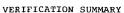
wrapped text (handwritten annotation)

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VERIFICATION SUMMARY                        DATE: 02/05/2001
PATENT APPLICATION:  US/09/757,100          TIME: 14:24:29

              Input Set : A:\isph-533.seq.asc
              Output Set: N:\CRF3\02052001\I757100.raw

L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:43 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-
DD,MMM-YYYY or Season-YYYY
L:48 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1
M:254 Repeated in SeqNo=1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
```

```
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:500 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:783 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:3
L:796 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4
L:809 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:5
L:822 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:6
L:830 M:283 W: Missing Blank Line separator, <220> field identifier
L:834 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7
L:847 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8
L:860 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9
L:873 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:10
L:886 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11
L:899 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:911 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13
L:924 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14
L:937 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15
L:950 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16
L:963 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17
L:971 M:283 W: Missing Blank Line separator, <220> field identifier
L:975 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:18
L:988 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19
L:1001 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:20
L:1014 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:21
L:1027 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22
L:1040 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:23
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:24
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:25
L:1078 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:26
L:1091 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:27
L:1104 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:28
L:1112 M:283 W: Missing Blank Line separator, <220> field identifier
L:1116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:29
L:1129 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:30
L:1142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:31
L:1155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:32
L:1168 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:33
L:1181 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:34
L:1193 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:35
L:1206 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:36
L:1219 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:37
L:1232 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:38
L:1245 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:39
```

VERIFICATION SUMMARY   DATE: 02/05/2001
PATENT APPLICATION: US/09/757,100   TIME: 14:24:29

    Input Set : **A:\isph-533.seq.asc**
    Output Set: **N:\CRF3\02052001\I757100.raw**

```
L:1253 M:283 W: Missing Blank Line separator, <220> field identifier
L:1257 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:40
L:1270 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:41
L:1283 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:42
L:1295 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:43
L:1311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1311 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:44
```